Diogo M. Camacho

SENIOR BIOINFORMATICS SCIENTIST

Wyss Institute for Biologically Inspired Engineering @ Harvard University

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Computational Systems Biology, Machine Learning, Bioinformatics

Qualifications and research interests

Formally trained biochemist with graduate and post-doctoral work in Computational Systems Biology, with a focus on network inference and machine learning. Industry experience in development and implementation of computational tools for omics data analysis, drug discovery and target identification. I have extensive experience in the analysis of diverse data types, from gene expression microarrays to next-generation sequencing, metabolomics and phosphoproteomics. I am interested in the application of machine learning/deep learning tools and techniques in the context of drug discovery, disease biology characterization, large data analytics for biology, while focused on bridging the gap between the computational and experimental labs through highly engaging and fruitful collaborations.

Technical Skills

Machine learning, multi omics, R/Bioconductor, keras, perl, Latex, python, MATLAB, awk, bash. Adept user of OS X/macOS, Unix. Familiarity with cloud computing architectures (AWS) and high performance computing environments.

Education

Virginia Polytechnic Institute and State University   *Blacksburg, VA*

PH.D. GENETICS, BIOINFORMATICS, AND COMPUTATIONAL BIOLOGY   *2002–2007*

- Thesis title: in silico cell biology and biochemistry – a systems biology approach

Faculdade de Ciencias da Universidade de Lisboa   *Lisboa*

B.SC. BIOCHEMISTRY   *1995–2001*

Experience

Wyss Institute @ Harvard University   *Boston, MA*

SENIOR BIOINFORMATICS SCIENTIST, ADVANCED TECHNOLOGY TEAM   *2016–Present*

- Lead the Systems Discovery Initiative at the Institute
- Development and implementation of research strategy for Systems Discovery group implementing ML/DL/AI capabilities
- Managerial and mentoring role, responsible for a team of computational biologists, bioinformaticians, data analysts
- Hands-on development of algorithms and computational approaches for dissemination internally and with corporate partners via R Shiny applications
- Responsible for the implementation of diverse tools for analysis of high throughput data (transcriptomics, RNA-seq, metabolomics, proteomics, 16S rDNA sequencing) in support of diverse grant work
- Involved in writing and managing federal grant applications and grant awards with DARPA, NIH

Evelo Biosciences   *Cambridge, MA*

SENIOR SCIENTIST, COMPUTATIONAL SYSTEMS BIOLOGY   *2015–2016*

- Lead Computational Systems Biology supporting preclinical development
- Responsible for the implementation of diverse tools for analysis of high throughput data (transcriptomics, RNA-seq, metabolomics) as well as a 16S rDNA sequencing analysis pipeline
- Responsible for the identification of novel therapeutic opportunities based on in-house and publicly available data
- Implemented analytical software tools to be used by bench scientists in R Shiny
- Responsible for the interface with IT provider to delineate and expand computational capabilities of the company, from general to research needs

Symbiota   *Cambridge, MA*

CONSULTANT, COMPUTATIONAL SYSTEMS BIOLOGY   *2014–2015*

- Developed an R Shiny application for the enrichment of pathways for plant transcriptomics

Ember Therapeutics *Watertown, MA*

Senior Scientist, Computational Systems Biology *2014*

- Lead Computational Systems Biology efforts. Responsible for the identification of novel target opportunities
- Responsible for the implementation of diverse tools for analysis of high throughput data (transcriptomics, RNA-seq, metabolomics)
- Implemented knowledge based and data driven construction of screening libraries for recombinant proteins, small peptides and RNAi
- Implemented analyses strategies (QC, statistical analyses, hit-calling) for high throughput screens
- Responsible for the implementation and maintenance of Ember Therapeutic portfolio management system and dissemination to senior scientific team
- Responsible for the interface with IT provider to delineate and expand computational capabilities of the company, from general to research needs

Pfizer, Inc *Cambridge, MA*

Senior Research Scientist, Computational Sciences Center of Emphasis *2011–2014*

- Developed and implemented a network analysis tool for the characterization of differential networks in healthy and diseased populations under the scope of metabolic diseases
- Developed and implemented a methodology for metabolite set enrichment analysis for metabolomics data
- Performed data analysis in transcriptomics, proteomics and metabolomics for different customers within the organization with particular emphasis in Cardiovascular and Metabolic diseases
- Performed analysis of genetic data (genome-wide and metabolome-wide) from large sets of patient cohorts
- Implemented network inference tools for the analysis of large-scale data sets
- Involved in project decision-making process for the characterization of toxicology patterns of drugs and drug candidates

Howard Hughes Medical Institute @ Boston University *Boston, MA*

Post-doctoral Fellow *2007–2011*

- Developed a network inference algorithm for identification of regulatory architectures of pathways
- Identified a novel mechanism of action for antifungal drugs using transcriptomics and metabolomics data
- Identified and characterized the small RNA regulatory network in bacterial systems using gene expression data
- Performed data analysis of gene expression data and metabolomics data in bacterial and fungal systems
- Consulted in the implementation and usage of inference algorithms across platforms for biotechnology/pharmaceutical companies in the Boston area
- Developed inference algorithm to study functional interactions in gene regulatory networks

Awards and Grants

Synergistic Discovery and Design (DARPA) *$2,000,000*

co-PI *9/1/17*

Publications

Si, L, Prantil-Baun, R, Benam, K, Bai, H, Rodas, M, Burt, M, Potla, R, Hasselkus, R, Camacho, DM, Ferrante, T, Collins, JJ, Ingber, DE, (2019), Influenza infection, evolution and therapeutic responses in a human airway chip, Nature, under review, NA

Jalili-Firoozinezhad, S, Gazzaniga, FS, Calamari, EL, Camacho, DM, Fadel, C, Nestor, B, Cronce, MJ, Tovaglieri, A, Levy, O, Gregory, KE, Breault, DT, Cabral, JMS, Kasper, DL, Novak, R, Ingber, DE, (2019), Complex human gut microbiome cultured in anaerobic human intestine chips, Nature Biomedical Engineering, in press, NA

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Camacho, DM, Collins, KM, Powers, RK, Costello, JC, Collins, JJ, (2018), Next-generation machine learning for biological networks, Cell, 173, 1581–1592

Musah, S, Dimitrakakis, N, Camacho, DM, Church, GM, Ingber, DE, (2018), Directed differentiation of human induced pluripotent stem cells into mature kidney podocytes and establishment of a Glomerulus Chip, Nature Protocols, 13, 1662–1685

Paandey, SP, Winkler, JA, Li, H, Camacho, DM, Collins, JJ, Walker, GC, (2014), Central role for RNase YbeY in Hfq-dependent and Hfq-independent small-RNA regulation in bacteria, BMC Genomics, 15, 121

Galagan, JE, Minch, K, Peterson, M, Lyubetskya, A, Azzizi, E, Sweet, L, Gomes, A, Rustad, T, Dolganov, G, Glotova, I, Abeel, T, Mawhinney, C, Kennedy, A, Allard, R, Brabant, W, Krueger, A, Jaini, S, Honda, B, Yu, W-H, Hickey, M, Zucker, J, Garay, C, Weiner, B, Sisk, P, Stolte, C, Winkler, J, Van de Peer, Y, Iazzetti, P, Camacho, D, Dreyfuss, J, Liu, Y, Dorhoi, A, Mollenkopf, H-J, Drogaris, P, Lamontagne, J, Zhou, Y, Piquenot, J, Park, ST, Raman, S, Kaufmann, S, Mohney, R, Chelsky, D, Moody, B, Sherman, D, Schoolnik, G, (2013), The Mycobacterium tuberculosis regulatory network and hypoxia, Nature, 499, 178–183

Belenky, P, Camacho, D, Collins, JJ, (2013), Fungicidal drugs induce a common oxidative-damage cellular death pathway, Cell Reports, 3, 350–358

Marbach, D, Costello, JC, Kuffner, R, Vega, N, Prill, RJ, Camacho, DM, Allison, KR, the DREAM5 Consortium, Kellis, M, Collins, JJ, Stolovitzky, G, (2012), Wisdom of crowds for robust gene network inference, Nature Methods, 9, 796–804

Dwyer, DJ, Camacho, DM, Callura, JM, Kohanski, MA, Collins, JJ, (2011), Antibiotic-induced bacterial cell death exhibits physiological and biochemical hallmarks of apoptosis, Molecular Cell, 46, 561–572

Modi, SR, Camacho, DM, Kohanski, MA, Collins, JJ, (2011), Functional characterization of bacterial sRNAs using a network biology approach, Proc. Natl. Acad. Sci. USA, 108, 15522–15527

Camacho, DM, Collins, JJ, (2009), Systems biology strikes gold, Cell, 137, 24–26

Camacho, D, Vera-Licona, P, Laubenbacher, R, Mendes, P, (2007), Comparison of existing reverse engineering methods by use of an in silico system, Ann. N. Y. Acad. Sci., 1115, 73–89

Mendes, P, Camacho, D, de la Fuente, A, (2005), Modelling and simulation for metabolomics data analysis, Biochem. Soc. Trans., 33, 1427–1429

Camacho, D, de la Fuente, A, Mendes, P, (2005), The origin of correlations in metabolomics data, Metabolomics, 1, 53-63

Martins, AM, Camacho, D, Shuman, J, Sha, W, Mendes, P, Shulaev, V, (2004), A systems biology study of two distinct growth phases of Saccharomyces cerevisiae cultures, Curr. Genomics, 5, 649–663